Amino Acid and nucleotide sequence of the murine OKT3 heavy chain variable region (Accession #A222621)

```
MERHWIFLLLSVTAGVHSQVQLQQSGAELARPGASVKMSCKASYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTN
YNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCARYYDDHYCLDYWGQGTTLTVSSAKTTAPSVYPLAPVCGD
TTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVD
KKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQ
TQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEMTKKQVTL
TCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFS
RTPGK
```

ORIGIN

```
  1 gaattcccct ctccacagac actgaaaact ctgactcaac atggaaaggc ctgatctt
 61 tctactcctg ttgtcagtaa ctgcaggtgt ccactcccag gtccagctgc agcagtctgg
121 ggctgaactg gcaagacctg gggcctcagt gaagatgtcc tgcaaggctt ctggctacac
181 ctttactagg tacacgatgc actgggtaaa acagaggcct ggacagggtc tggaatggat
241 tggatacatt aatcctagcc gtggttatac taattacaat cagaagttca aggacaaggc
301 cacattgact acagacacac cctccagcac agcctacatg caactgagca gcctgacatc
361 tgaggactct gcagtctatt actgtgcaag atattatgat catattact gccttgacta
421 ctggggccaa ggcaccactc tcacagtctc ctcagccaaa acaacagccc catcggtcta
481 tccactggcc cctgtgtgtg gagatacaac tggctcctcg gtgactctag gatgcctggt
```

FIG. 1A

```
 541 caagggttat ttccctgagc cagtgacctt gacctggaac tctgatccc  tgtccagtgg
 601 tgtgcacacc ttccagctg  tcctgcagtc tgacctctac accctcagca gctcagtgac
 661 tgtaacctcg agcacctggc ccagccagtc catcacctgc aatgtggccc acccggcaag
 721 cagcaccaag gtggacaaga aaattgagcc cagaggggcc acaatcaagc cctgtcctcc
 781 atgcaaatgc ccagcaccta acctcttggg tggaccatcc gtcttcatct tccctccaaa
 841 gatcaaggat gtactcatga tctccctgag cccatagtc  acatgtgtgg tggtggatgt
 901 gagcgaggat gacccagatg tccagatcag ctggtttgtg aacaacgtgg aagtacacac
 961 agctcagaca caaacccata gagaggatta caacagtact ctccgggtgg tcagtgccct
1021 cccatccag  caccaggact ggatgagtgg caaggagttc aaatgcaagg tcaacaacaa
1081 agacctccca gcgcccatcg agagaaccat ctcaaaaccc aaagggtcag taagagctcc
1141 acagtatat  gtcttgcctc caccagaaga agagatgact aagaaacagg tcactctgac
1201 ctgcatggtc acagacttca tgcctgaaga catttacgtg gagtggacca acaacgggaa
1261 aacagagcta aactacaaga acactgaacc agtcctggac tctgatggtt cttacttcat
1321 gtacagcaag ctgagagtgg aaaagaagaa ctgggtggaa agaaatagct actcctgttc
1381 agtggtccac gagggtctgc acaatcacca cacgactaag agcttctccc ggactccggg
1441 taaatgagct cagcaccccac aaaactctca ggtccaaaga gacacccaca ctcatctcca
1501 tgcttccctt gtataaataa agcaccccagc aatgcctggg accatgtaaa aaaaaaaaaa
1561 aaaggaattc
```

FIG. 1A (Cont.)

Amino Acid and nucleotide sequence of the murine OKT3 light chain
variable region (Accession #A22259)

MDFQVQIFSFLLISASVIISRGQIVLTQSPAIMSASPGEKVTMTCSASSSVSYMNWYQQKSGTSPKRWIYD
TSKLASGVPAHFRGSGSGTSYSLTISGMEAEDAATYYCQQWSSNPFTFGSGTKLEINRADTAPTVSIFPPS
SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSY
TCEATHKTSTSPIVKSFNRNEC

ORIGIN

```
  1 gaattcccaa agacaaaatg gatttttcaag tgcagatttt cagcttcctg
    ctaatcagtg
 61 cctcagtcat aatatccaga ggacaaattg ttctcaccca gtctccagca
    atcatgtctg
121 catctccagg ggagaaggtc accatgacct gcagtgccag ctcaagtgta
    agttacatga
181 actggtacca gcagaagtca ggcacctccc ccaaaagatg gatttatgac
    acatccaaac
241 tggcttctgg agtccctgct cacttcaggg gcagtgggtc tgggacctct
    tactctctca
301 caatcagcgg catggaggct gaagatgctg ccacttatta ctgccagcag
    tggagtagta
361 acccattcac gttcggctcg gggacaaagt tggaaataaa ccgggctgat
    actgcaccaa
421 ctgtatccat cttcccacca tccagtgagc agttaacatc tggaggtgcc
    tcagtcgtgt
```

FIG. 1B

```
481 gcttcttgaa caacttctac cccaagaca tcaatgtcaa gtggaagatt
    gatggcagtg
541 aacgacaaaa tggcgtcctg aacagttgga ctgatcagga cagcaaagac
    agcacctaca
601 gcatgagcag caccctcacg ttgaccaagg acgagtatga acgacataac
    agctatacct
661 gtgaggccac tcacaagaca tcaacttcac ccattgtcaa gagcttcaac
    aggaatgagt
721 gttagagaca aaggtcctga gacgccacca ccagctccca gctccatcct
    atcttccctt
781 ctaaggtctt ggaggcttcc ccacaagcgc ttaccactgt tgcggtgctc
    taaacctcct
841 cccacctcct tctcctcctc ctccctttcc ttggctttta tcatgctaat
    atttgcagaa
901 aatattcaat aaagtgagtc tttgccttga aaaaaaaaa aaa
```

FIG. 1B (Cont.)

Hind111   BamH1

P   S   I   VH or VK   I
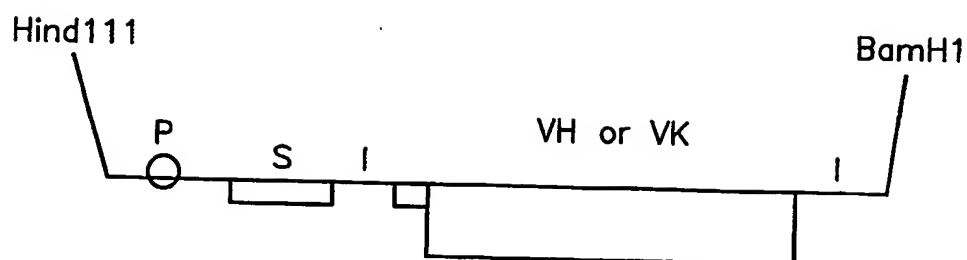
P	Mouse heavy chain Ig promoter
S	Signal peptide sequence
I	Intron

FIG. 2

OKT3 VH gene construct.   Nucleic Acid and amino acid sequences of murine

Seq. ID No 1
HindIII
AAGCTTATGAATATGCAAATCCTCTGAATCTACACATGGTAAAATATAGGTTTGTCTATACCACAAACAGAAAAACATGAGATCACAGTTCTCTCTACAGTTACTGAGCACAC
TTCGAATACTTATACGTTTAGGAGACTTAGATGTACCATTTATATCCAAACAGATATGGTGTTTGTCTTTTTGTACTCTAGTGTCAAGAGAGATGTCAATGACTCGTCGTG   110

NcoI
AGGACCTCACCATGGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTAAGGGGCTCACAGTAGCAGGCTTGAGGTCTCTGGACATATATATGGGTGACAA
TCCTGGAGTGGTACCCTACCTCGACATAGTAGGAGAAGAACCATCGTTGTCGATGTCCATTCCCGAGTGTCATCGTCCGACCTGTATATATACCCACTGTT   220

                                                M G W S C I I L F L V A T A T
                                                └──Signal

Seq. ID No 2

                                                                                                     PvuII
TGACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAGCTGCAACAGTCTGGGGCTGAACTCCGCAAGACCTGGGGCCTCAGTGAAGATGTCCTGCAAGG
ACTGTAGGTGAAACGGAAACGGAAAGAGAGGTGTCCACAGGTGTCCAGGTCGAGGGTCCACAGCGTTCTGGACCCCGGAGTCGTTCTCACGGACGTTCC   330

Seq. ID No 29 ──►   G V H S Q V Q L Q Q S G A E L A R P G A S V K M S C K
                     └──Signal   VH

FIG. 3

CTTCTGGCTACACGTTTACTAGGTACACGATGCACTGGGTAAAAACAGAGGCCCTGGACAAGGTTTGGAATGGATTGGATATACATTAACCCTAGCCGTGGATATACTAATTAC
GAAGACCGATGTGCAAATGATCCATGTGCTACGTGACCCATTTGTCTCCGGACCCGTTCCAAACCTTACCTAACCTTACCTAACCTATATGTAATTGGGATCGGCACCTATATGATTAATG 440

A S G Y T F T R Y T M H W V K Q R P G Q G L E W I G Y I N P S R G Y T N Y
CDRH1 — VH
CDRH2

AATCAGAAGTTCAAGGACAAGGCCACACTGACTACAGACAAATCTTCCAGCACACGCCTACAGCCTACATGCAACTGAGCAGCCTGACATCTGAGGACTCCGCAGTCTATTACTGTGC
TTAGTCTTCAAGTTCCTGTTCCGGTGTGACTGATGTCTGTTTAGAAGGTCGTCGGATGTACGTTGACTCGTCGGCGTCAGATAATGACACG 550

N Q K F K D K A T L T T D K S S S T A Y M Q L S S L T S E D S A V Y Y C A
CDRH2 — VH

AAGATATTATGATGATCATTACTGTCTCGACTACTGGGGCCCAAGGCACCACTTTGACAGTCTCCTCAGGTGAGTCCTTACAACCTCTCTTCTATTCAGCTTAAAATAGA
TTCTATAATACTACTAGTAATGACAGAGCTGATGACCCCGGTTCCGTGGTGAAACTGTCAGAGAGTCCACTCAGGAATGTTGGAGAGAAGATAAGTCGAATTTATCT 660

R Y Y D D H Y C L D Y W G Q G T T L T V S S
VH
CDRH3

FIG. 3 (Cont.)

FIG. 3 (Cont.)

OKT3 VL gene construct.

Nucleic acid and amino acid sequences of murine

Seq. ID No 3
HindIII

```
AAGCTTATGAATATGCAAATCCTCTGAATCTACACATGGTAAAATATAGGTTTGTCTATACCACAAACAGAAAAACATGAGAATCACAGTTCTTCTCTACAGTTA
TTCGAATACTTATACGTTTAGGAGACTTAGAGTGTACCATTTATATCCAAACAGATATGGTGTTGTCTTTTGTACTCTAGTGTCAAGAGAGATGTCAAT
                                                                                      100
```

Ncol

```
CTGAGCACACAGGACCTCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTAAGGGGCTCACAGTAGCAGGCTTGAGGTCTG
GACTCGTGTGTCCTGGAGTGGTACCCTACCTCGACATAGTAGGAGAAGAACCATCGTTGTCGATGTCCATTCCCGAGTGTCCGAACTCCAGAC
                                                                                      200
                                                  M  G  W  S  C  I  I  L  F  L  V  A  T  A  T
Seq. ID No 4 →                                      └─────────── Signal ───────────
```

```
GACATATATATGGGTGACAATGACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCAT
CTGTATATATACCCACTGTTACTGTAGGTGAAACGGAAAGAGAGGTGTCCACAGGTGTGGGTTTAACAAGAGTGGGTCAGAGAGTCGTTAGTACAGACGTA
                                                                                      300
                                              G  V  H  S  Q  I  V  L  T  Q  S  P  A  I  M  S  A
Seq. ID No 30 →                                └─ Signal ─┘ └─ VK
```

Kpnl

BstEll

```
CTCCAGGGGGAAAAGGTCACCATGACATGCAGTGCCAGCTCAAGTGTAAGTTACATGAACTGTACCAGCAGAAGTCAGGCACCTCCCCAAAAGATGGAT
GAGGTCCCCTTTTCCAGTGGTACTGTACGTCACGGTCGAGTTCACATTCAATGTACTTGACATGGTCGTCGTCTTCAGTCGTGGAGGGGTTTTCTACCTA
                                                                                      400
```

FIG. 4

S P G E K V T M T C S A S S S V S Y M N W Y Q Q K S G T S P K R W I
　　　　　　　　　　　　　　　　VK

TTATGACACATCAAAAACTGGCTTCTGGAGTACGGCTCACTTCAGGGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCTCAGGGATGGAAGCTGAA
++
AATACTGTGTAGTTTTGACCGAAGACCTCATGCCGAGTGAAGTCCCCGTCACCCAGAGAGTGTTAGAGTCCCTACCTTCGACTT
　　　　　CDRL1

Y D T S K L A S G V P A H F R G S G S G T S Y S L T I S G M E A E
　　　　　　　　　　　　　　　　　VK

GATGCCCGCAACTTATTACTGCCAGCAGTGGTCAAGTAACCATTCACGTTCGGAGTCTGGTACAAAGTTGGAAATCAAACGTGAGTAGAATTAAAACTTTG
++
CTACGGGCGTTGAATAATGACGGTCGTCACCAGTTCATTGGGTAAGTGCAAGCCTCAGACCATGTTTCAACCTTTAGTTTGCACTCTTAAATTTGAAAC
　　　CDRL2

D A A T Y Y C Q Q W S S N P F T F G S G T K L E I K
　　　　　　　　　　　　　　VK
　　　　　　　　　　　　　　　　CDRL3

　　　　BamHI
CTTCCTCAGTTGGATCC   617
++++++++++++++
GAAGGAGTCAACCTAGG

FIG. 4 (Cont.)

SUBSTITUTE SHEET (RULE 26)

Schematic map of the vector Apex-1 3F4V$_H$HuGamma4.

1 Afl III
1 Mlu I
22 Spe I
Ssp I 5942   257 Nde I
PVu I 5507   362 SnaB I
610 EcoR I
914 Hind III
924 Msc I
1019 Sal I
793   1043 BamH I
ATG 1057 1046 BspE I
APEX-1 3F4 VH Hugamma4 1408 Spl I
+   1572 Age I
6058 base pairs 1763 1671 BstE II
Unique Sites
2153
L1   2189
2307 1960 PflM I
2637
Xcm I 3802   2734
Bcl I 3646   357 2392 Pmi I
2645 Dra III
Cla I 3255
Bsm I 3203
Xba I 3118
Xho I 3106
PaeR7 I 3106
Eag I 3100
Not I 3099

FIG. 5A

Vector sequence (APEX-1 3F4V$_H$HuGamma4)

```
ACGGGTTGACATTGACTAGTTATTATTATAGTAATCAATTACGGGGTCATTAGGGT
GACCCCGCCCCATTGACGTCAATAATGACGTATGTTCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCCGCCTGGCTGAC    130
TGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGT    260
GATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGT    390
CGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGAATTCTGTTGGCGTCGCGGTTGATTACAAACTCTTCGCGG    520
TCTTTCCAGTACTCTTGGATCGGAAACCCGTCTGCGGCCTCGCCGACCTCGGCGCTCCGCCACCGGAGAGTCCGAGGGAGTCCGAGCGGCCGAGCCAAACCTCTGTGGGGTGAGTACTCCCTCTCAA    650
TCAAGCTTGAGGTGTGGCAGGCTTGAGATCTGGCCATACACCTTGATATTCACCTGGCCCGTCTGGACAATGACATCACCTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAGCTGCAGCAGTCTGGGG    780
GGATCCGGACCATCATGAAGTGAGCCATCATGTTTCTCTTTCTCCTGTCAGTAACTGCCCGGGCTCCGGCCTTTATTCCTGGAATGATTGGGGTCTGGAATGTGTGTAAAAACAGGACCTGGACAGTGGTAAAACAGAACAGGCCCTGGACAGTGGT    910
GGATCCGGACCATCATGAAGTGAGCCATCATGTTTCTCTTTCTCCTGTCAGTAACTGCCGGGGCTCCGGCCTTTATTCCTGGAATGATTGGGGTCTGGAATGTGTG    1040
Seq. ID No 6  M K N S W V I L F L L S V T A G V H S | Q V Q V Q Q S G A E L A R P W A S V K    1170
                            Signal ─────┘            └──── 3F4Vh ─────
```

```
S C K A S G Y N F N S Y N M Q W V K Q R P G Q G L E W I G A I Y P G D T S Y T Q    1300
└──────────────── 3F4Vh ──────────────────┘
```

```
K F R G K A T L T A D K S S S T A Y M Q L S S L A S E D S A V Y Y C A R R T V G G Y F D    1430
└─────────────────────── 3F4Vh ───────────────────────────┘
```

```
Y W G Q G T T L T V S S | A S T K G P S V F P L A P C S R S T S E S T A A L G C L V K D    1560
└── 3F4Vh ──┘           └──────────────── hG4CH1 ───────────────┘
```

```
Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S S    1690
└──────────────────────── hG4CH1 ────────────────────────┘
```

```
S L G T K T Y T C N V D H K P S N T K V D K R V    1820
└──────────────── hG4CH1 ─────────────────┘
```

```
                                                                                      1950
                                                                                      2080
```

FIG. 5B

ACTTCCACTTCCCCTCAGTCTCAGACCTTCTCTCCTCCCCAGATCTGAGTAACTCCCAAATCTTCTTCTCTGCGAGTCCAAATATGGTCCCCATGCCCATCATGCCCAGTAAGCCAACCCAGGCCCTCGCC 2210

Seq. ID No 31 →
E S K Y G P P C P S C P
hG4Hinge

CTCCAGCTCAAGGCGGGAGCAGGTGCCCCAGCCGGGTGCTGACGCATCCACCTCACCTCTTCCTCAGCCACCTGAGTTCCTGGGGGGACCATCAGTCTTCCT 2340

Seq. ID No 32 →
A P E F L G G P S V F L
hG4CH2

AATCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCAT 2470

F P P K P K D T L M I S R T P E V T C V V V D V S Q E D P E V Q F N W Y V D G V E V H
hG4CH2

AATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCC 2600

A K T K P R E E Q F N S T Y R V V S V L T V L H Q D W L N G K E Y K C K V S N K G L
hG4CH2

TCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCACGGGGTGCGAGGGCCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAG 2730

Seq. ID No 33 →
S S I E K T I S K A K
hG4CH2

G Q P R E P Q V Y T L P P S Q E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S
hG4CH3

2860

AATGGGCAGCCGGAGAACAACTACAAGACCACACCACCTGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTCTCATGCTCC 2990

N G Q P E N N Y K T T P P V L D S D G S F F L Y S R L T V D K S R W Q E G N V F S C S
hG4CH3

GTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGGTAAATGAGTGCCAGGGCCGGCAAGCCCCCGCTCCCCATCCATCACACTGGGGCCGGCCTCGAGCCATGCATCT 3120

V M H E A L H N H Y T Q K S L S L S L G K
hG4CH3

AGAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGT 3250

CTGGATCGATCCCGCCATGGTCAACGCCATATTTCTATTTACAGTAGGGACCTTCGTTCGTTGTGTGAGGTACCGCTGTATTCCTAGGGAAATAGTAGAGGCACCTTGAACTGTCTGCATCAGCCATATAG 3380

FIG. 5B (Cont.)

```
GSCCCGCCTGTTCGACTTACAAACACAGGCACAGTACTGACAAACCCATACACCTCCTCTGAAATACCCATAGTTGCTAGGGCTGTCTCCGAACTCATTACACCCTCCAAAGTCAGAGCTGTAATTTCGCC  3510
GTCAAGGGCAGCGAGGGCTTCTCCGACTACTTCTGCCGAGAGTAGACACTTCAGCTAATCCCTGCAGGGTAGACACTTCAGCTAATCCCTGATGAGGTCTACTAGAATAGTCAGTGCGGCTCCCATTTGAAAATTCAC  3640
GGACTTGATCAGCTTCAGAAGATGCCGGAGGGCCTCCAACACAGTAATTTTCCTCCCGACTCTTAAATAGAAAATGTCAAGTGGACTAAGCAGGAAGTGGACTAACTCATTACTACTGACAACAGCTGTTTTTTT  3770
GCTTTTTAATTAGTTGCTAGGCAACGCCCCTCCAGAGGGCGTGTTGGTTTTGCAAGAGAGAAGAGAGGCATTGTAGAGGCTTCCGCCATCCGCCCAGTTGTCAAAACAGGACTGCTTCTATTTCTGTCACACTGTCTGGCCC  3900
GCTCACAAGTCCAGCACACTCCATACCCCCTTTAATAAGCAGTTTGGGAACGGGTGCGGGTCTATTCCGCCTCTCGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTCAGAGGCTTTTGGAGGCTAGGCTTTTTGGAGGCTAGGCTTTTTATTTATTATGCAGAGGGTGCGGGTCTATTCCGCCTCTCGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTCAGAGG  4030
GGCGGGTTGCTGCTCTGGCGTTTTTCCATAGGCTCCGCCCCTGACGAGCATCACAAAAATCGACGCTCAGAGGTGGGCGCTTTCTCCCTTCGGGAGGCGTTTCCCCCTGGGAGCTCCC  4160
GGGTTGAGGCTGTGTGCAGTAGTAGGCGGTGCTACAGAGTTCTTGAAGTGGCGGTCTACAGAGTTCTTGAAGTGGCGTATCGTCTTGAGTCCAACCCGTAACTATCGTCTTGAGTCCAACCCGTAAGCTGCTCTCCAA  4290
GCAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGCGGTGCTACAGAGTTCTTGAAGTGGCGTATCGTCTTGAGTCCAACCCGTAACTATCGTCTTGAGTCCAACCCGTAAGCTGGTAACAGGATTAGC  4420
GTTGATCCGGGGCAAACAAACCACCCGCTGGTAGCCGGTGGTTTTTTGTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAGATCTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAA  4550
GGATGCTTAAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTGACTCCCCGTAGATAACAGATACGGAGGGCTTACCATCTGGCCCAGTGCTGCAATGA  4680
GGCGGCGAGACCCCACGCGCTCACCGGCTCCAGATTAATCAGCAATAAACCAGCCGAGGGCCGAAGGCCGAGGGCCAGCCGAGAAGTGGTCCTGCACAGCCATCGTGGTAGTTTGCCAACGTTGTTGCCGCAGCCATCGTGGTAGTTTGCCAACGTTGT  4810
TTGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAAGTGTGTTGCCTCCTTCGGTCCTCCCTGTTTGGTATGGCTTCATTCAGTATGGCTTCATTCAGTATCACTCATGGTTATGCGCAGCACTCATGGTTATGCGCAGCAC  4940
GAATCCCCCATGTTGTGCAAAAAAGCCGGTTAGCTCGTTGACTGGTGAGTACTCAACCAAGTCATTCTGAGTACTCAACCAAGTCATTCTGAGATACTGTGTCCCGCGGTTATCACTCATGCCGCGGTTATCACTCATGCCGCGCGTCAATACGGGAT  5070
AGTGCTTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTCGAAGGATCTTCAAGGATCTTCAAGGATCTTCAGACTCAGGGGCACCCACTTCGGGCTTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTGTTGAGATCCAGTTCGATGTAACCCAC  5330
TCTTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTACTTTCACCAGCGTT  5850
GCGGATACACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTG  5980
```

GCGGATACACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTG 6058

FIG. 5B (Cont.)

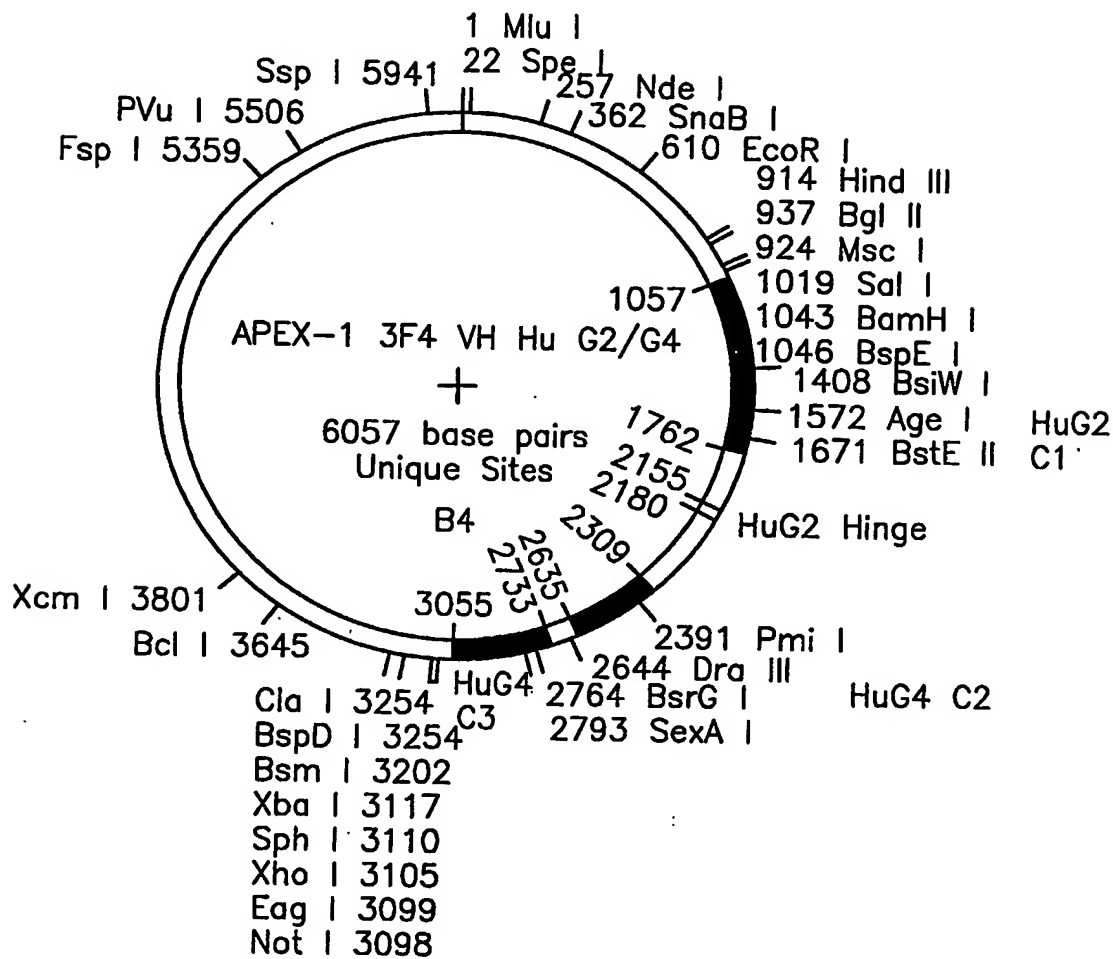Schematic map of the vector Apex-1 3F4V$_H$HuG2/G4.

FIG. 6A

Vector Sequence (APEX-13F4V_H HuG2/G4)

ACGCGTTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGCCCCGCCTGGCTG 120
ACCGCCCAACGACCCCCGCCATTGACGTCAATAAGTACGGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACTTGGC 240
AGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACAT 360
CTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAG 480
TTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGT 600
GAACCGTCAGATCTCGTTGGGCTGTCGGGGTTGATTACAAACTCTTGCCGGTCTTTCCAGTACTCTTGGGGGTGATCGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACAT 720
CAGTCCGCCATCGACCGGATCGGAAAACCCTCGACGTTGGGCGCCTTTGAGTGCTTCTCGCCATGACTTCTCGCCTAAGATTGTCAGTTTCCAAAAACGTGAGGAGGATTTGATAT 840
CACCTGGCCCGCCGGGTGATGCCTTTGAGGGTGGCCGCGTCCATCTGGTCAGAAAGACAATCTTTTTGTTGTCAAGCTTGAGGTGTGGCAGGTTGGCCATACACTTGAGTGA 960
AATGACATCCACTTTGCCTTTCTCTCCACAGTGTCCACTCCCAGTGCCTTGGGCTGCAGGTGTCCAGTCCACTCCAGTCGTGTGGGCCGGGTCCAGTTCAGGTTGGGTTATTCTC 1080

(Seq. ID No: 8) → M K W S W V I L
                              └── Signal ──┘

TCCCTCCTGTCAGTAACTGCCGGGCGTCCACTCCCAGTGTTCAGGTTCAGGTCCAGCAGTCTGGGCCTGAGCTGGCAAGACCCTGGGCTTCAGTGAAGTTGTCCTGCAAGGCTTCCTGCGCTGCAAGTGTCTGCTCTGAAGT... 1200
ATAGTTACTGGATGCAGTGGGTAAAAACAGAGGCCTGGACAGGGTCTGGAATGGGCTATTATCCTGGAGATGGTGATACTAGCTACACTCAGAAGTTCAGGGGCAAGGCCACA 1320
NSYWMQWVKQRPGQGLEWIGAIYPGDGDTSYTQKFRGKAT
                                              └────── 3F4Vh ──────┘
TTGACTGCAGATAAATCCTCCAGCACAGCCTACATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGACGTTAGGAGGCGTACGGTTAGGAGGCTACTTTGACTACTGGGGC 1440
LTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGYFDYWG
                                              └────── 3F4Vh ──────┘
CAAGGCACCACTCTCACAGTCTCCTCAGCGTCTTCCCCCCTGGCGCCCTGCTCCAGGAGCACTCCGAGAGCACAGCCGCCCTGGGCTGCCTGGTCAAGGAC 1560
QGTTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKD
                  └─ 3F4Vh ─┘ └─────── G2G4CH1 ───────┘

FIG. 6B

TACTTCCCCGAACCGGTGACGGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTG 1680
Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V
—G2G4CH1—

CCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGAGGAGGGTGTCTGCTGGA 1800
P S S N F G T Q T Y T C N V D H K P S N T K V D K T V
—G2G4CH1—

TGGCCAGGCTCAGCCCTCCTGCCTGGACGCGTGTGCAGCCCGGCCCCAGCCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTCATGCTCAG 1920
C C V E C P P C P —Hinge—

AATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCCTGCCCCTCCAGCTCAAGGGCGGGGACAGGTGCCCATCCAGGACAGCCCCAGCTGGGTGCT 2280
C C V E C P P C P —Hinge—

(Seq. ID No: 35)→ A P P V A G P S V F L F P P K D T L M I S R T P E V T C V
—G2G4CH2—

ACACGTCCACCTCCATCTCTTCCTCAGCACCTGTGCAGGACCGTCAGTCTTCTGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGCGTG 2400
(Seq. ID No: 34)→ E R —Hinge—

GTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTACCGTGTG 2520
V V D V S Q E D P E V Q F N W Y V D G V E V H N A K T K P R E E Q F N S T Y R V
—G2G4CH2—

GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGG 2640
V S V L T V L H Q D W L N G K E Y K C K V S N K G L P S S I E K T I S K A K
—G2G4CH2—

FIG. 6B (Cont.)

ACCCACGGGGTGCGAGGGCCACACGGACAGAGAGGCCAGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGACCCCACAGGTGTACAC 2760

(Seq. ID No: 36) → G Q P R E P Q V Y T
                                 G2G4CH3

CCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA 2880
L P P S Q E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N
               G2G4CH3

GTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGA 3000
Y K T T P P V L D S D G S F F L Y S R L T V D K S R W Q E G N V F S C S V M H E
               G2G4CH3

GGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCCAGGCCGGCCAAGCCCCCGCTCCCCATCCATCACACTGGCCGGCCGCTCGAGCATGCATCTA 3120
A L H N H Y T Q K S L S L S L G K .
               G2G4CH3

GAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATC 3240
TTATCAGTGTCTGGATCGATCCCGCCATGGTATCAACGCCATATTTCTATTTTACAGTAGGGACCCTCTTCGTTGTGTGTAGGTACCGCTGTATTCCTAGGGAAATAGTAGAGGCCACCTTGAACT 3360
CTCCAAAGTCAGAGCTGTAATTTCGCCATCAAGGGCAGCGAGGGCTTCACCATAGTTGTCTCCGAGAGTCCGTAAGGTAGACACTTCAGCTAATCCCTCGATGAGGTCT 3480
TCTAGAAATAGTAGTCAGTGCGGCTCCCATTTGAAAATTCACTTACTTGATCAGCTTCAGAGAGATGGCGGAGGGCCTCCAACACAGTAATTTCCTCCCGACTCTTAAAATAGAAAATGTCAA 3600
CACCCAGGCCTAGAATGTTCCACCCAATCATTACTATGACAACAGCTGTTTTCTGTCACACAGCTGCTTCTATTTCTGTCCCTGCTCGGGACCCCTGGGCCCTGGCGCCCGCTTACTCTGCCCTGCTACTCTGCCCTTAATAAGCAGTTTGGGAAC 3840
GGGTGGCGGGTCTTACTCCGCCATCCCGCCCTACCTGCTTCCCGCCCCATGGCTGCCGAGCCGGTTGCTGGTTTTCCATAGGCTCC 3960
GCTATTCCAGAAGTAGTGAGGAGGCTTTTTGGGCCCTAGGCTTTGCAAAAAGGAGCTCCCAGCAAAAGCCTAAAAAGCCCGTTGCTGGGGTTTTCCATAGGCTCC 4200
GCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGA 4440

FIG. 6B (Cont.)

CCTGCCGCCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCCGTGGGCGCCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTTAGTCGTTCGCTCCAAGCTGGGCTGTG 4560
CCACGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCGTAAGACACGACTTATCGCCAACCCGGTAACACCAGGATTAGCA 4680
AGCGGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGGCCTAACTACCGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGAAGCCAGTTACCTTCGGAAAAAGAG 4800
TGGTAGCTCTTGATCCGGCAAACAAACCACCCGCTGGTAGGCGGTGGTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGG 4920
GGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAGTTATCAAAAAGGATCTTCACCTAGATCCTTTAAATAAAATGAAGTTTTAAATCAATCTAAAGTA 5040
CATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGA 5160
TACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTC 5280
GCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAA 5400
GTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAGTCATTCTGAG 5520
AATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCT 5640
CAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATG 5760
GCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTA 5880
TTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTG 6057

FIG. 6B (Cont.)

Map of the heavy chain expression vector pSVgptHuG2/G4 used in
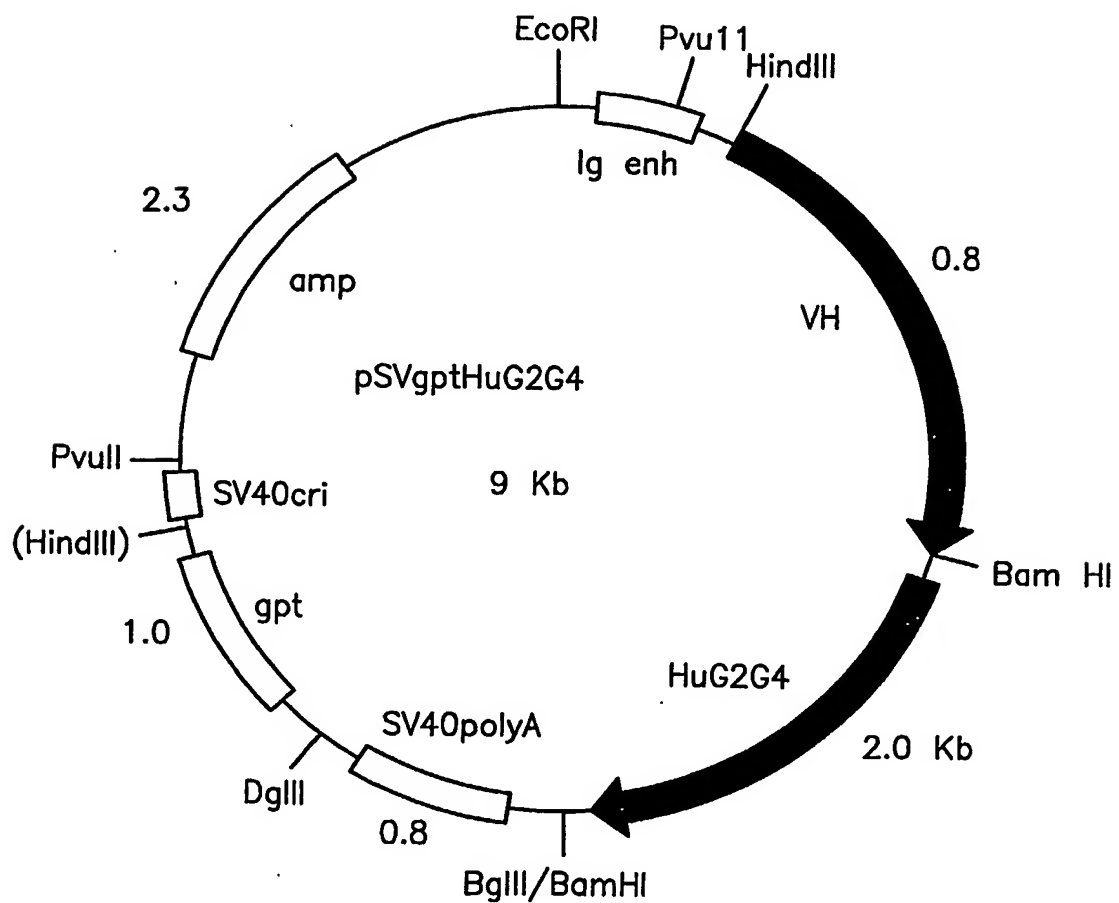

FIG. 7

(Seq. ID No. 9) ———→ Bam HI

5' untranslated
intron from
native IgG4

GGATCCTCTAGATTGAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTGGG
GGCAGGGAGGGGGCTAAGGTGACGCAGGTGGCGCCAGCCAGGTGCACACCC
AATGCCCATGAGCCCAGACACTGGACCCTGCATGGACCATCGCGGATAGACA
AGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGGTC
ACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCCGTCTTCCCCC
TGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCT
GGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA
CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC
TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACA
GTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTC
AGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCA
AGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTCATG
CTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGGAGGCACAGG
CTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCA
GACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACC
CCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGA
TCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGC
CCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGG
ACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTG
ACACGTCCACCTCCATCTCTTCCTCAGCACCACCTGTGGCAGGACCGTCAGTC
TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGA
GGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTC
AACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGG
GAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGC
ACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
GCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCA
CGGGGTGCGAGGGCCACATGGACAGAGGTCAGCTCGGCCCACCCTCTGCCCT
GGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAGCCA
CAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCA
GCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCT
GGACTCCGACGGCTCCTTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGC
AGGTGGCAGGAGGGGAATGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGGTAAATGAGTGCC

3' untranslated region
from native IgG4

AGGGCCGGCAAGCCCCCGCTCCCCGGGCTCTCGGGGTCGCGCGAGGATGCTT
GGCACGTACCCCGTCTACATACTTCCCAGGCACCCAGCATGGAAATAAAGCA
CCCACCACTGCCCTGGGCCCCTGTGAGACTGTGATGGTTCTTTCCACGGGTCA
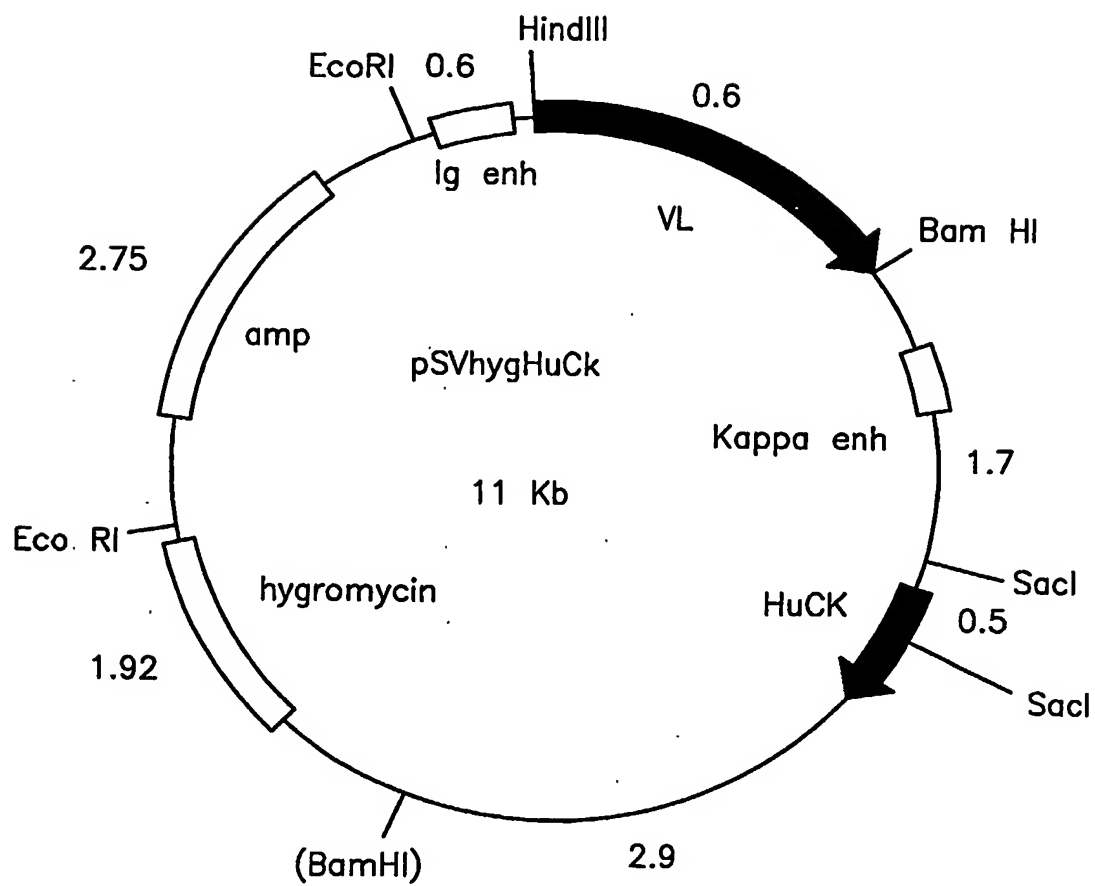GGCCGAGTCTGAGGCCTGAGTGACATGAGGaAttCAGAtctGGatCC

Bgl II

FIG. 8

Map of the light chain expression vector pSVgptHuCK

FIG. 9

Amino Acid sequences of DeImmunised OKT3 heavy chain variable regions

		1									10									20									30		
(Seq. ID No. 10)	1	Q V Q L Q Q S G A E L A R P G A S V K M S C K A S G Y T F T																													OKT3 MoVH
(Seq. ID No. 11)	1	Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T A T																													OKT3 DIVHv1
(Seq. ID No. 12)	1	Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T A T																													OKT3 DIVHv2
(Seq. ID No. 13)	1	Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T A T																													OKT3 DIVHv3
(Seq. ID No. 14)	1	Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T A T																													OKT3 DIVHv4
(Seq. ID No. 15)	1	Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T																													OKT3 DIVHv5
(Seq. ID No. 16)	1	Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T																													OKT3 DIVHv6
(Seq. ID No. 17)	1	Q V Q L V Q S G A E V K K P G A S V K V S C K A S G Y T F T																													OKT3 DIVHv7

		40									50									60		
	31	R Y T M H W V K Q R P G Q G L E W I G Y I N P S R G Y T N Y																				OKT3 MoVH
	31	R Y T M H W V R Q A P G Q G L E W I G Y I N P S R G Y T N Y																				OKT3 DIVHv1
	31	R Y T M H W V R Q A P G Q G L E W I G Y I N P S R G Y T N Y																				OKT3 DIVHv2
	31	R Y T M H W V R Q A P G Q G L E W I G Y I N P S R G Y T N Y																				OKT3 DIVHv3
	31	R Y T M H W V R Q A P G Q G L E W I G Y I N P S R G Y T N Y																				OKT3 DIVHv4
	31	R Y T M H W V R Q A P G Q G L E W I G Y I N P S R G Y T N Y																				OKT3 DIVHv5
	31	R Y T M H W V R Q A P G Q G L E W I G Y I N P S R G Y T N Y																				OKT3 DIVHv6
	31	R Y T M H W V R Q A P G Q G L E W I G Y I N P S R G Y T N Y																				OKT3 DIVHv7

FIG. 10

FIG. 10 (Cont.)

Top alignment block (residues 61–90):

	61																												90	
OKT3 MoVH	N Q K F K D K A T L T T D K S S S T A Y M Q L S S L T S E D
OKT3 DIVHv1	A Q K F Q D R V T I T T D K S S S T A Y L Q M N S L K T E D
OKT3 DIVHv2	A D S V K G R F T I T T D K S S S T A Y L Q M N S L K T E D
OKT3 DIVHv3	N Q K F K D R V T I T T D K S S S T A Y L Q M N S L K T E D
OKT3 DIVHv4	N Q K F K D R V T I T T D K S S S T A Y L Q M N S L K T E D
OKT3 DIVHv5	N Q K F Q D R V T I T T D K S S S T A Y L Q M N S L K T E D
OKT3 DIVHv6	A Q K F Q D R V T I T T D K S S S T A Y L Q M N S L K T E D
OKT3 DIVHv7	N Q K F K D R V T I T T D K S S S T A Y L Q M N S L K T E D

Bottom alignment block (residues 91–~113):

	91							100											110					
OKT3 MoVH	S A V Y Y C A R Y Y D D H Y C L D Y W G Q G T T L T V S S
OKT3 DIVHv1	T A V Y Y C A R Y Y D D H Y C L D Y W G Q G T T V T V S S
OKT3 DIVHv2	T A V Y Y C A R Y Y D D H Y C L D Y W G Q G T T V T V S S
OKT3 DIVHv3	T A V Y Y C A R Y Y D D H Y C L D Y W G Q G T T V T V S S
OKT3 DIVHv4	T A V Y Y C A R Y Y D D H Y C L D Y W G Q G T T V T V S S
OKT3 DIVHv5	T A V Y Y C A R Y Y D D H Y C L D Y W G Q G T T V T V S S
OKT3 DIVHv6	T A V Y Y C A R Y Y D D H Y C L D Y W G Q G T T V T V S S
OKT3 DIVHv7	T A V Y Y C A R Y Y D D H Y C L D Y W G Q G T T V T V S S

Amino Acid sequences of DeImmunised OKT3 light chain variable regions

```
(Seq. ID No. 18)  1   QIVLTQSPAIMSASPGEKVTMTCSASSSVS    OKT3 MoVK
(Seq. ID No. 19)  1   QIVLTQSPATLSLSPGERATLTCSASSS[A]S  OKT3 DIVKv1
(Seq. ID No. 20)  1   QIVLTQSPATLSLSPGERATLTCSASSSVS    OKT3 DIVKv2

                 31   YMNWYQQKSGTSPKRWIYDTSKLASGVPAH    OKT3 MoVK
                 31   YMNWYQQKPGKAPKRWIYDTSKLASGVPSR    OKT3 DIVKv1
                 31   YMNWYQQKPGKAPKRWIYDTSKLASGVPSR    OKT3 DIVKv2

                 61   FRGSGSGTSYSLTISGMEAEDAATYYCQQW    OKT3 MoVK
                 61   FSGSGSGTDYSLTINSLEAEDAATYYCQQW    OKT3 DIVKv1
                 61   FSGSGSGTDYSLTINSLEAEDAATYYCQQW    OKT3 DIVKv2

                 91   SSNPFTFGSGTKLEIN                  OKT3 MoVK
                 91   SSNPFTFGQGTKVEIK                  OKT3 DIVKv1
                 91   SSNPFTFGQGTKVEIK                  OKT3 DIVKv2
```

FIG. 11

OLIGOS FOR CONSTRUCTION OF DIVHs   (SEQ ID NOS: 37-57)

```
KTDIVH1     GAAGTCAAGAAACCTGGGGCCTCAGTGAAGGTGTCCTGCAAGG
KTDIVH2
       GCCCCAGGTTTCTTGACTTCAGCCCCAGACTGTACCAGCTGGACCTG
KTDIVH3     TGGGTAAGACAGGCGCCTGGACAAGGTTTGG
KTDIVH4     GTCCAGGCGCCTGTCTTACCCAGTGCATC
KTDIVH4A
       AGGCGCCTGTCTTACCCAGTGCATCGTGTACCTAGTAGCCGTGTAGCC
KTDIVH5     CAATCAGAAGTTCAAGGACAGGGTCACAATCACTACAGACAAA
KTDIVH5A    CGCTCAGAAGTTCCAGGACAGGGTCACAATCACTACAGACAAA
KTDIVH5B    CGCTGACAGTGTCAAGGGCAGGTTCACAATCACTACAGACAAA
KTDIVH5C    CAATCAGAAGGTCAAGGACAGGTTCACAATCACTACAGACAAA
KTDIVH6     GTCCTTGAACTTCTGATTGTAATTAGTATATCCACGG
KTDIVH6A    GTCCTGGAACTTCTGAGCGTAATTAGTATATCCACGG
KTDIVH6B    GCCCTTGACACTGTCAGCGTAATTAGTATATCCACGG
KTDIVH6C    GTCCTTGACCTTCTGATTGTAATTAGTATATCCACGG
KTDIVH7     AGCCTGAAAACTGAGGACACCGCAGTCTATTACTG
KTDIVH8     GTCCTCAGTTTTCAGGCTGTTCATTTGCAAGTAGGCTGTGCT
KTDIVH9     CCAAGGCACCACTGTGACAGTCTCCTCAGG
KTDIVH10    CCTGAGGAGACTGTCACAGTGGTGCCTTGG
KT3VHY      GGTGTCCACTCCCAGGTCCAGCTG
KT3VHZ      CAGCTGGACCTGGGAGTGGACACCTGTGG
VHVK1       GCATGTTGACCCTGACGCAAGCTTATGAATATGCAAA
VH12 GCGATAGCTGGACTGAATGGATCCTATAAATCTCTG
```

OLIGOS FOR CONSTRUCTION OF DIVKs   (SEQ ID NOS: 58-74)

```
KTDIVK1    CCCTCTCTCTTTCTCCAGGGGAACGCGCCACCTTGACATGCAGTG
KTDIVK2    CCTGGAGAAAGAGAGAGGGTTGCTGGAGACTGGGTG
KTDIVK3
       CATGAACTGGTACCAGCAGAAGCCCGGCAAAGCTCCCAAAAGATGGAT
KTDIVK4    CGGGCTTCTGCTGGTACCAGTTCATGTAACTTACACTT
KTDIVK4A       CTTCTGCTGGTACCAGTTCATGTAACTTGCACTTGAGC
KTDIVK5
       GGGTCTGGGACCGATTACTCTCTCACCATCAATAGTCTGGAAGCTGAAG
KTDIVK6
       GTAATCGGTCCCAGACCCACTGCCACTGAAGCGAGACGGTACTCCAG
KTDIVK7    TTCACGTTCGGACAAGGTACAAAGGTGGAAATCAAACG
KTDIVK8    CTTTGTACCTTGTCCGAACGTGAATGGGTTACTTGACC
KKT22      GCGGATCCAGTCGACGAAGCA
KT3VKX     CTGAATGGATCCAACTGAGGAAGCAAAGTTTAAATTCTACTCACG
KT3VKY     CAAATTGTTCTCACCCAGTCTCCAGCAA
KT3VKZ     TTGCTGGAGACTGGGTGAGAACAATTTGGGAG
KT3VKZ2    TGGAGACTGGGTGAGAACAATTTGGGAGTGGACACCTGTGG
KT3VKZ3    AGAGAGGGTTGCTGGAGACTGGGTGAGAACAATTTG
VHVK1      GCATGTTGACCCTGACGCAAGCTTATGAATATGCAAA
VK12 GCGATAGCTGGACTGAATGGATCCAACTGAGGAAGC
```

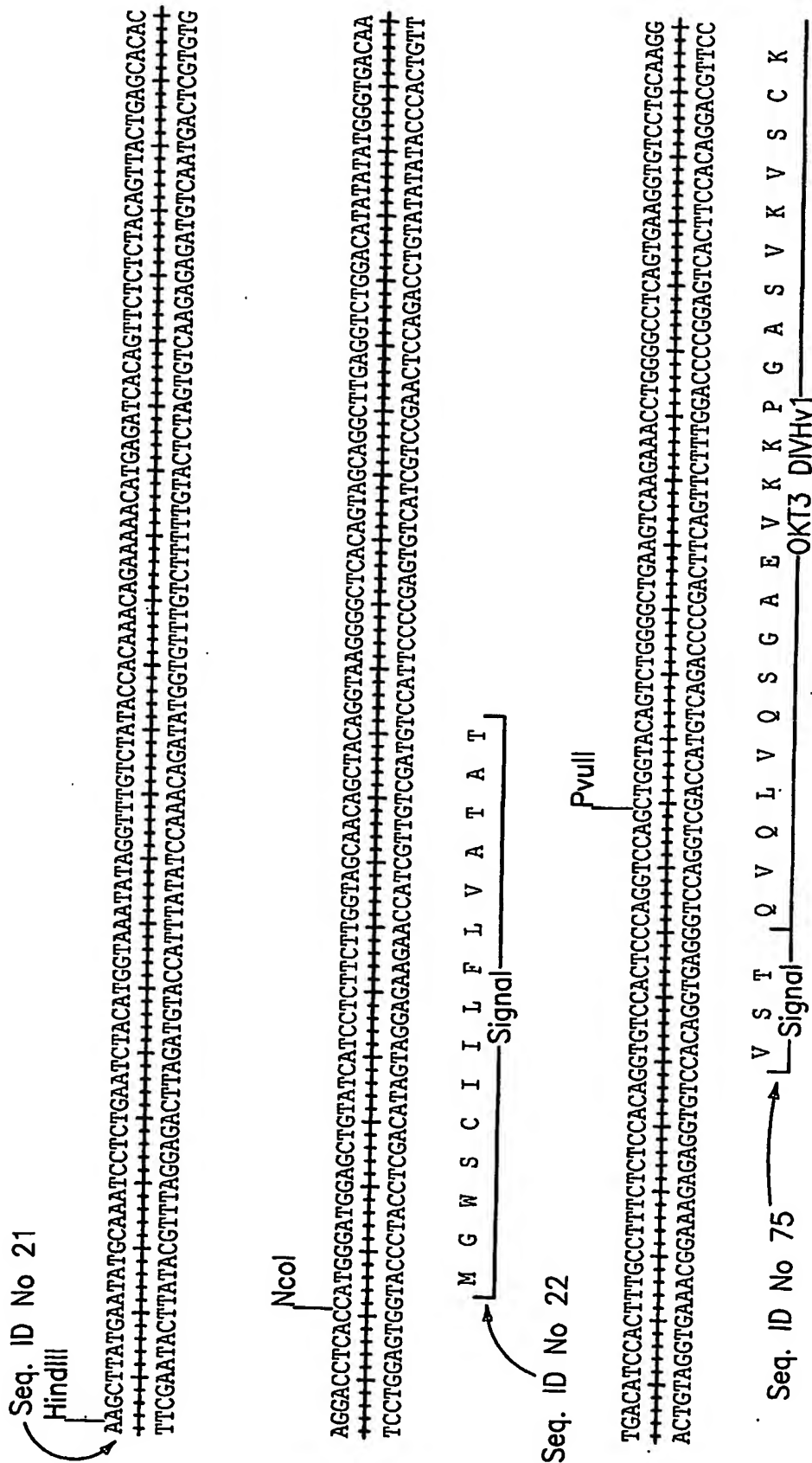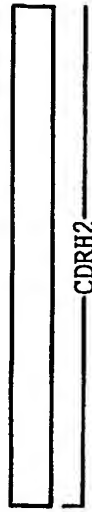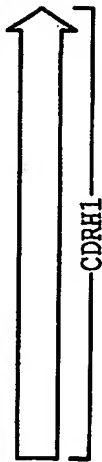DNA and Amino acid sequence of DeImmunised OKT3 VH version 1.

Seq. ID No 21
HindIII
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TTCGAATACTTATACGTTTAGGAGACTTAGATGTGTACCATTTATATATCCAAACAGATATGTGTTTGTCTTTTGTACTGTGTCAGAGAGATGTCAATGACTCGTGTG

Ncol
AGGACCTCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTAAGGGGCTCACAGTAGCAGGCTTGAGGTCTGGACATATATATGGGTGACAA
TCCTGGAGTGGTAGCCCTACCTCGACACTAGTAGGAGAGAACCATCGTTGTCGATGTCCATTCCCGAGTGTCATCGTCCGAACTCCAGACCTGTATATATACCCACTGTT

       M   G   W   S   C   I   I   L   F   L   V   A   T   A   T
      └───── Signal ─────┘
Seq. ID No 22

PvuII
TGACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTGTCCAGGTCCCAGCTGGTGCAGTCTGGGGCTGAAGTCAAGAAACCTGGGGCCTGAGTGTCCTGCAAGG
ACTGTAGGTGAAACGGAAAGAGAGGTGTCCACAGGTGTCCACAGGTCGACCACCGTCAGACCCCGACTTCAGTTCTTTGGACCCCGGACTCACTTCCACAGGACGTTCC

     V   S   T   Q   V   Q   L   V   Q   S   G   A   E   V   K   K   P   G   A   S   V   K   V   S   C   K
Seq. ID No 75   └─Signal─┘└──────────────── OKT3 DIVHv1 ────────────────┘

FIG. 13

SUBSTITUTE SHEET (RULE 26)

CTTCTGGCTACACGGCTACTAGGTACACGATGCACTGGGTACGAGGCGCCTGGACAAGGTTTGGAATGGATACATTAACCCTAGCCGTGGATATACTAATTAC

GAAGACCGATGTGCCGATGATCCATGTCCACGTGCTACGTGACCCATTCTGTCCGCGGACCTGTTCCAAACCTTACCTAACCTATGTAATTGGGATCGGCACCTATATGATTAATG

A S G Y T A T R Y T N H W V R Q A P G Q G L E W I G Y I N P S R G Y T N Y
OKT3 DIVHv1

CDRH1　　　　　CDRH2

GCTCAGAAGTTCCAGGACAGGGTCACAATCACTACAGACAAATCTTCCAGCACCAGCCTACTTGCAAATGAACAGCCTGAAAACTGAGGACACCGCAGTCTATTACTGTGC

CGAGTCTTCAAGGTCCTGTCCCAGTGTTAGTGATGTCGTGTTAGAAGGTCGTGTCGGATGAACGTTTACTTGTCGGACTTTGACTCCTGTGGCGTCAGATAATGACACG

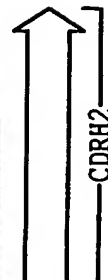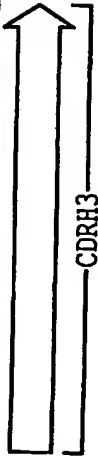A Q K F Q D R V T I T T D K S S S T A Y L Q M N S L K T E D T A V Y Y C A
OKT3 DIVHv1

CDRH2

FIG. 13 (Cont.)

AAGATATTATGATGATCATTACTGTCTCGACTACTGGGGCCAAGGCACCACTCTGGGGCCAAGGCACCACTCTGTGACAGTCTCCTCAGGTGAGTCCTTACACAACCTCTCTCTTCTATTCAGCTTAAATAGA
++
TTCTATAATACTACTAGTAATGACAGAGCTGATGACCCGGTTCCGTGGTGACACTGTCAGAGGAGTCCACTCCTCAGAGGAGTCACTCAGGAATGTTGGAGAGAGAGATAAGTCGAATTTATCT

R Y Y D D H Y C L D Y W G Q G T T V T V S S
└────OKT3─DIVHv1
        └────CDRH3────┘

TTTTACTGCATTTGTTGGGGGGGAAAATGTGTGTATCTGAATTTCAGGTCAGGTCATGATGAAGGACACCTTGGGAGTCAGAAAGGGTCATTGGGAGCCCGGCCTGATGCAG
++
AAAATGACGTAAACAACCCCCTTTACACACATAGACTTAAAGTCCAGTTCCGATCCCTGTGGAACCCTCAGTCTTTCCCAGTAACCCTCGGGCCCGACTACGTC

                                        Xmal
                                          Smal

                          BamHI
ACAGACATCCTCAGCTCCCAGACTTCATGGCCAGAGATTTATAGGATCC   819
++
TGTCTGTAGGAGTCGAGGGTCTGAAGTACCGGTCTCTAAATATCCTAGG

FIG. 13 (Cont.)

DNA and Amino Acid Sequence of Deimmunised OKT3 VK version 1.

Seq. ID No 23
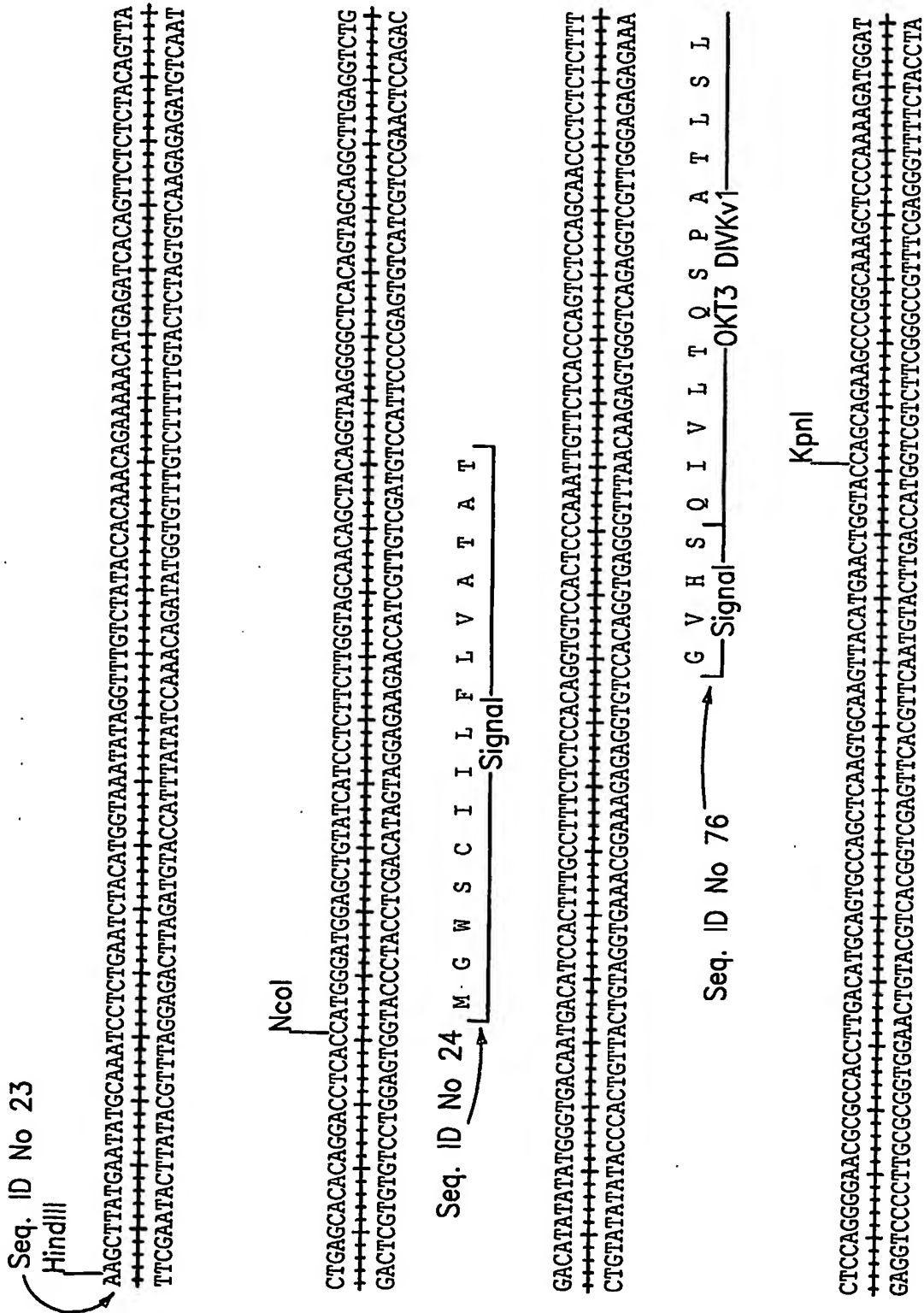HindIII
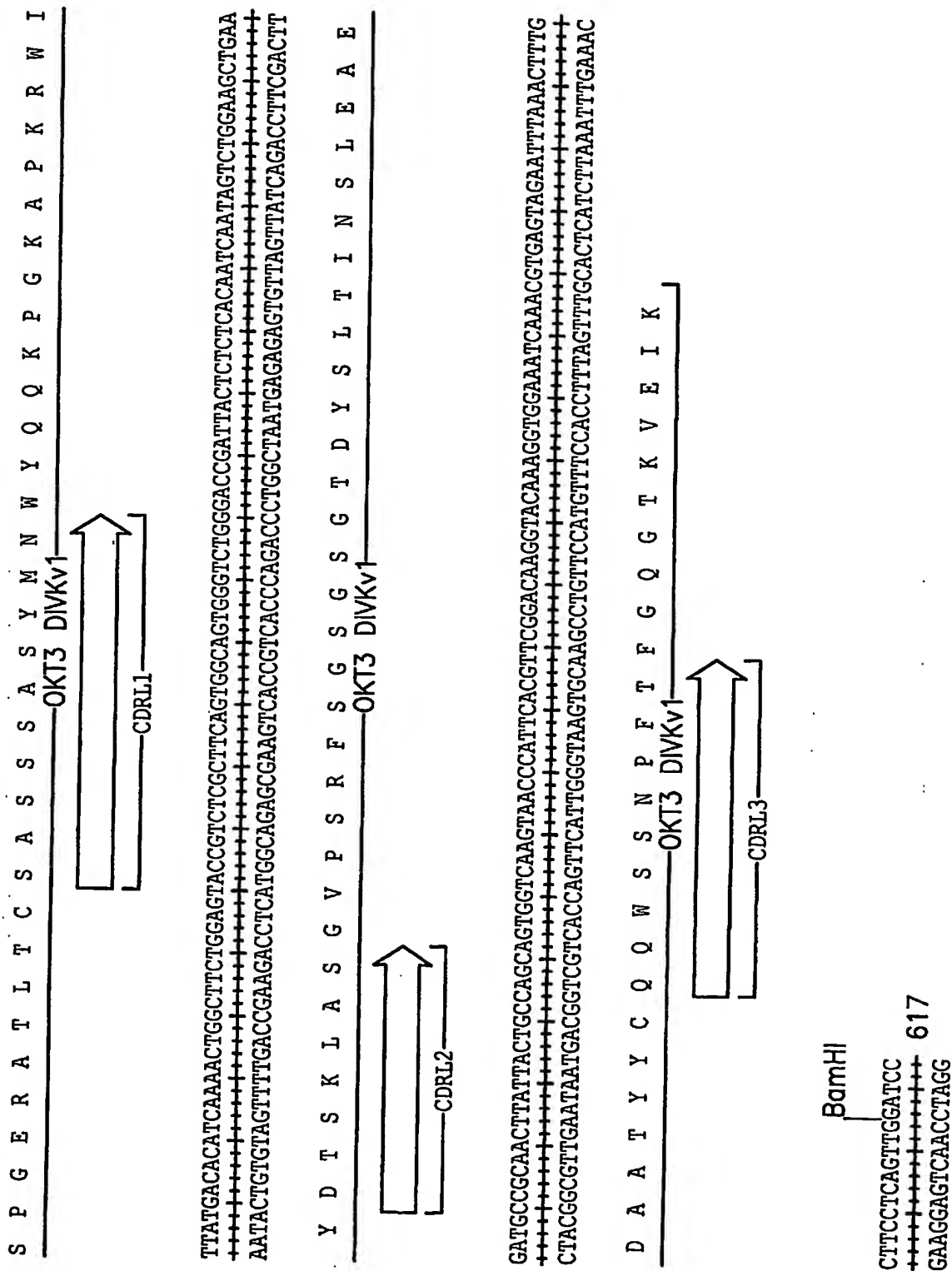
AAGCTTATGAATATGCAAATCCTCTGAATCTACATGGTAAAATATAGGTTTGTCTATACCACAAACAGAAAAACATGAGATCACACAGTTCTCTCTACAGTTA
+----+
TTCGAATACTTATACGTTTAGGAGACTTAGATGTACCATTTTATATCCAAACAGATATGGTTGTCTTTTTGTACTCTAGTGTGTCAAGAGAGATGTCAAT

NcoI

CTGAGCACACAGGACCTCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTAAGGGCTCACAGTAGCAGGCTTGAGTCTG
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+
GACTCGTGTGTCCTGGAGTGGTACCCTACCTCGACATAGTAGGAGAGAACCATCGTTGTCGATGTCATTCCCGAGTGTCATCGTCCGAACTCCAGAC

Seq. ID No 24   M G W S C I I L F L V A T A T
                └——————————————Signal——————————————┘

GACATATATATGGGTGACAATGACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAAATTGTTCTCACCCAGTCTCCAGCAACCCTCTCTCTTT
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+
CTGTATATATACCCACTGTTACTGTAGGTGAAACGGAAAGAGAGGTGTCCACAGGTGAGGGTTTAACAAGAGTGGGTCAGAGTCGTTGGGAGAGAGAAA

Seq. ID No 76   G V H S Q I V L T Q S P A T L S L
                       └——Signal——┘└——————————OKT3 DIVKv1——————————

                                                    KpnI

CTCCAGGGGAACGCGCCACCTTGACAATGCAGTGCCAGCTCAAGTGCAAGTTACATGAACTGGTACCAGCAGAAGCCCGGCCAAAGATGGAT
+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+----+
GAGGTCCCCTTGCGCGGTGGAACTGTTACGTCACGTCGAGTTCACGTTCAATGTACTTGACCATGGTCGTCTTCGGGCCGGTTTCTACCTA

FIG. 14

S P G E R A T L T C S A S S S A S Y M N W Y Q Q K P G K A P K R W I
OKT3 DIVKv1
CDRL1

TTATGACACATCAAAAACTGGCTTCTCTGGAGTACCGTCTCGCTTCAGTGGCAGTGGGTCTGGGACCGATTACTCTCTCACAATCAATAGTCTGGAAGCTGAA
AATACTGTGTAGTTTTTGACCGAAGAGCGAAGCTCACCGTCACCCAGACCCTCGCCTAATGAGAGAGTGTTAGTTATCAGACCTTCGACTT

Y D T S K L A S G V P S R F S G S G S G T D Y S L T I N S L E A E
OKT3 DIVKv1
CDRL2

GATGCCGCAACTTATTACTGCCAGCAGTGGTCAAGTAACCCATTCACGTTCGGACAGGGTACCAAGGTGGAAATCAAACGTGAGTAGAATTTAAACTTTG
CTACGGCGTTGAATAATGACGGTCGTCACCAGTTCATTGGGTAAGTGCAAGCCTGTCCCATGTTTCCACCTTTAGTTTGCACTCATCTTAAATTTGAAAC

D A A T Y Y C Q Q W S S N P F T F G Q G T K V E I K
OKT3 DIVKv1
CDRL3

BamHI
CTTCCTCAGTTGGATCC —617
GAAGGAGTCAACCTAGG

FIG. 14 (Cont.)

Murine and Chimaeric OKT3 binding to Jurkat, JRT3 and HPB-ALL

cells
Values represent the positive % of gated cells in M1

Cell Type	Passage #	Murine OKT3	Mouse Isotype Control	Chimaeric OKT3	Human Isotype Control
Jurkat	12	81.20	0.5	94.68	0.44
JRT3	14	3.45	0.26	4.56	0.43
HPB-ALL	10	99.63	0.62	99.39	0.29

FIG. 15

Antibody	Clone No.	% Cells in M1	
		HPB−ALL	JRT3
Chimaeric OKT3	N/A	99.74	7.74
Control no OKT3 no PE	N/A	2.22	2.3
Control no OKT3 with PE	N/A	2.3	2.21
DMEM Control	N/A	1.91	2.42
DIVH1/DIVK1	19D6	93.87	2.16
DIVH2/DIVK1	24C12	28.47	2.34
DIVH3/DIVK1	27F6	84.75	2.28
DIVH4/DIVK1	30F7	93.06	2.65
DIVH5/DIVK1	35F2	98.15	2.77
DIVH6/DIVK1	37E9	97.85	3.08
DIVH7/DIVK1	42E7	98.62	3.12

FIG. 16

Table 3:

| Antibody	Clone No.	% Cells in M1	
		HPB−ALL	JRT3
Chimaeric OKT3	N/A	99.95	0.1
Control no OKT3 no PE	N/A	0.1	0.02
DIVHv1/DIVK2	48G3	20.18	0.1
DIVHv2/DIVK2	52B8	90.04	0.25
DIVHv3/DIVK2	55G5	84.73	0.14
DIVHv4/DIVK2	55B2	69.26	0.13
DIVHv6/DIVK2	66C6	98.16	0.53
DIVHv7/DIVK2	70G10	95.57	0.66

FIG. 17

Competition assay. Inhibition of binding biotinylated mouse OKT3 by
chimaeric and DeImmunised OKT3 antibodies, DIVHv1/DIVKv1, DIVHv3/DIVKv1,
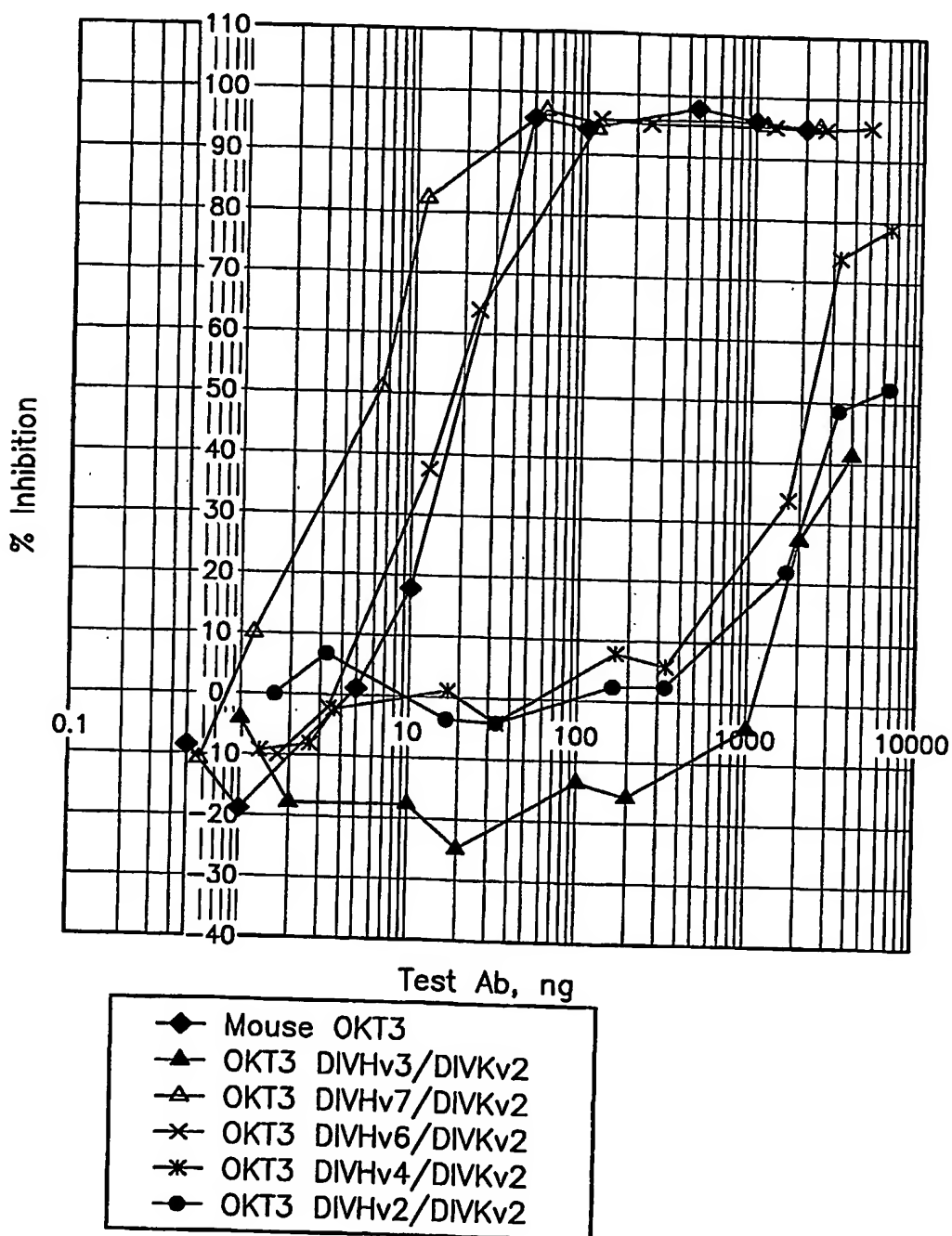DIVHv5/DIVKv1, DIVHv6/DIVKv1, OKT3DIVH7/DIVKv1.
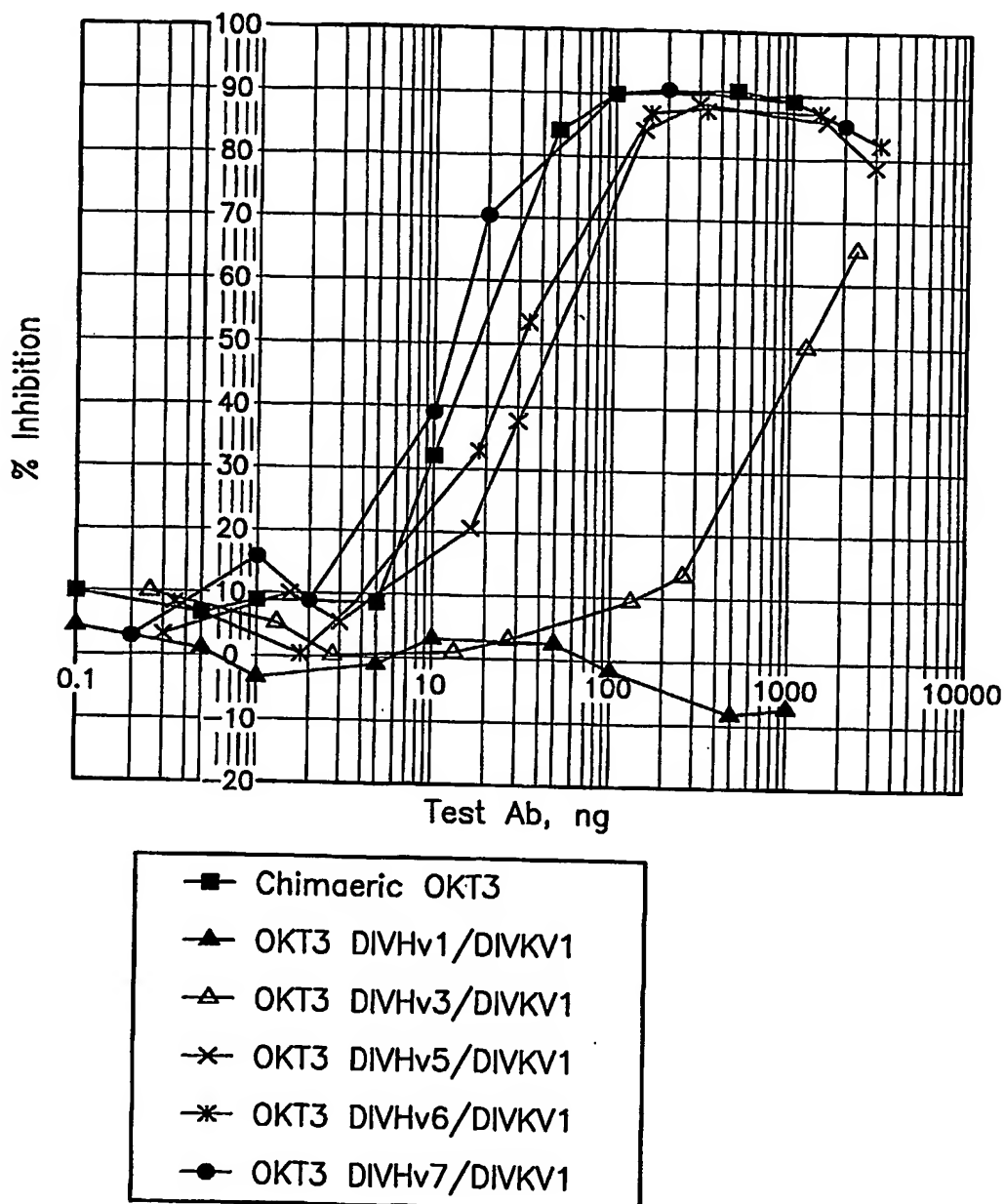
FIG. 18

Competition assay. Inhibition of binding biotinylated mouse OKT3 by
mouse, chimaeric and DeImmunised OKT3 antibodies DIVHv2/DIVKv1,
DIVHv4/DIVKv1.
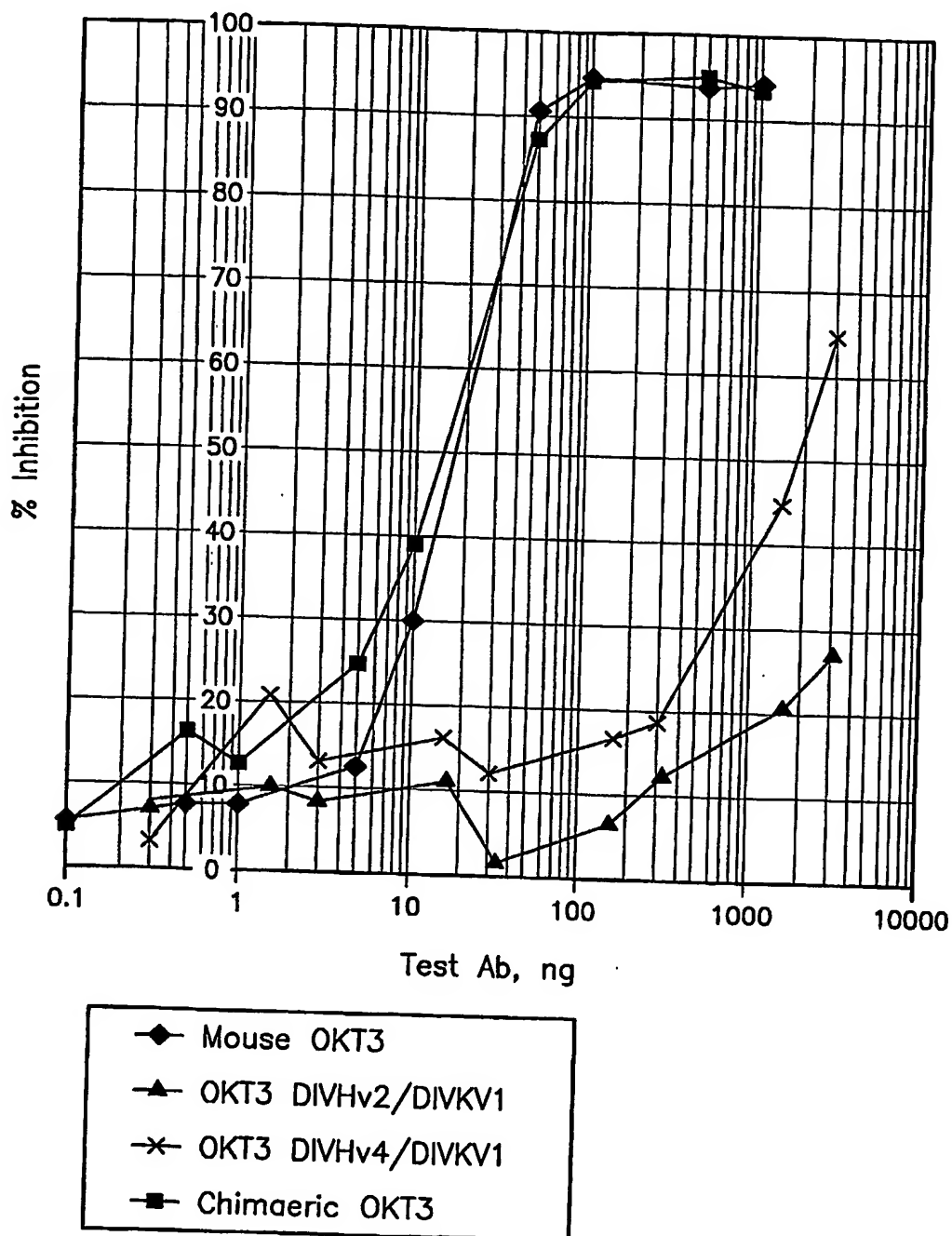
FIG. 19

Competition assay. Inhibition of binding biotinylated mouse OKT3 by mouse, chimaeric and DeImmunised OKT3 antibodies DIVHv3/DIVKv2, DIVHv7/DIVKv2.

FIG. 20

Competition assay. Inhibition of binding biotinylated mouse OKT3 by mouse, chimaeric and DeImmunised OKT3 antibodies DIVHv1/DIVKv2, DIVHv1/DIVKv1, DIVHv5/DIVKv2, DIVHv5/DIVKv1.

Legend:
- ◆ Mouse OKT3
- ▲ OKT3 DIVHv1/DIVKv2
- △ OKT3 DIVHv1/DIVKv1
- ✕ OKT3 DIVHv5/DIVKv2
- ✱ OKT3 DIVHv5/DIVKv1
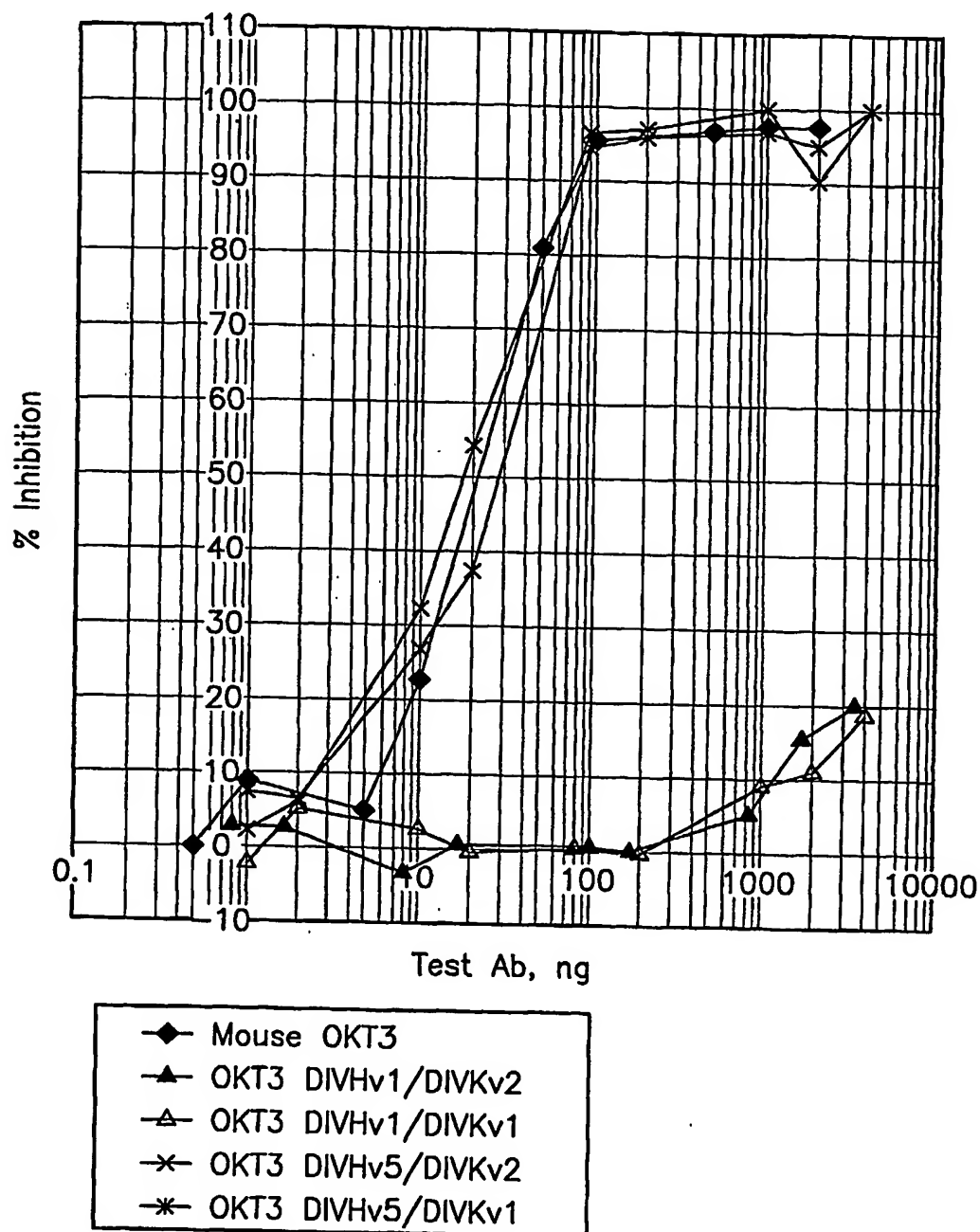
FIG. 21

The IC₅₀ determinted from these plots are shown in Table 4.

Table 4:

ANTIBODY	IC50 (ng)
Murine OKT3 1	18
Murine OKT3 2	19
Murine OKT3 3	20
Chimeric OKT3 1	18
Chimeric OKT3 2	15
Di-immunized OKT3 DIVHv1/DIVKv1	N/A
Delm OKT3 DIVHv1/DIVKv1 2nd prep	>2000
De-immunized OKT3 DIVHv2/DIVKv1	>3000
De-immunized OKT3 DIVHv3/DIVKv1	1250
De-immunized OKT3 DIVHv4/DIVKv1	1900
De-immunized OKT3 DIVHv5/DIVKv1	45
Delm OKT3 DIVHv5/DIVKv1 2nd prep	19
De-immunized OKT3 DIVHv6/DIVKv1	30
De-immunized OKT3 DIVHv7/DIVKv1	12
De-immunized OKT3 DIVHv1/DIVKv2	>2000
De-immunized OKT3 DIVHv2/DIVKv2	>3000
De-immunized OKT3 DIVHv3/DIVKv2	>4000
De-immunized OKT3 DIVHv4/DIVKv2	2100
De-immunized OKT3 DIVHv5/DIVKv2	28
De-immunized OKT3 DIVHv6/DIVKv2	18
De-immunized OKT3 DIVHv7/DIVKv2	6

FIG. 22